

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 22:44:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671996.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR21671996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671996_1.fastq.gz SRR21671996_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 22:44:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	286,922,860
Mapped reads	283,503,164 / 98.81%
Unmapped reads	3,419,696 / 1.19%
Mapped paired reads	283,503,164 / 98.81%
Mapped reads, first in pair	141,794,327 / 49.42%
Mapped reads, second in pair	141,708,837 / 49.39%
Mapped reads, both in pair	282,639,654 / 98.51%
Mapped reads, singletons	863,510 / 0.3%
Secondary alignments	0
Supplementary alignments	3,933,451 / 1.37%
Read min/max/mean length	15 / 150 / 150.22
Duplicated reads (estimated)	143,185,864 / 49.9%
Duplication rate	39.67%
Clipped reads	142,274,796 / 49.59%

2.2. ACGT Content

Number/percentage of A's	10,811,352,118 / 27.77%
Number/percentage of C's	7,680,091,042 / 19.73%
Number/percentage of T's	11,716,165,398 / 30.09%
Number/percentage of G's	8,726,724,561 / 22.41%
Number/percentage of N's	658,086 / 0%

GC Percentage	42.14%
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2.3. Coverage

Mean	12.5833
Standard Deviation	264.4274

2.4. Mapping Quality

Mean Mapping Quality	54.08
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2.5. Insert size

Mean	136,853.72
Standard Deviation	3,669,140.47
P25/Median/P75	237 / 287 / 333

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	402,646,539
Insertions	5,654,809
Mapped reads with at least one insertion	1.91%
Deletions	9,860,265
Mapped reads with at least one deletion	3.37%
Homopolymer indels	46.53%

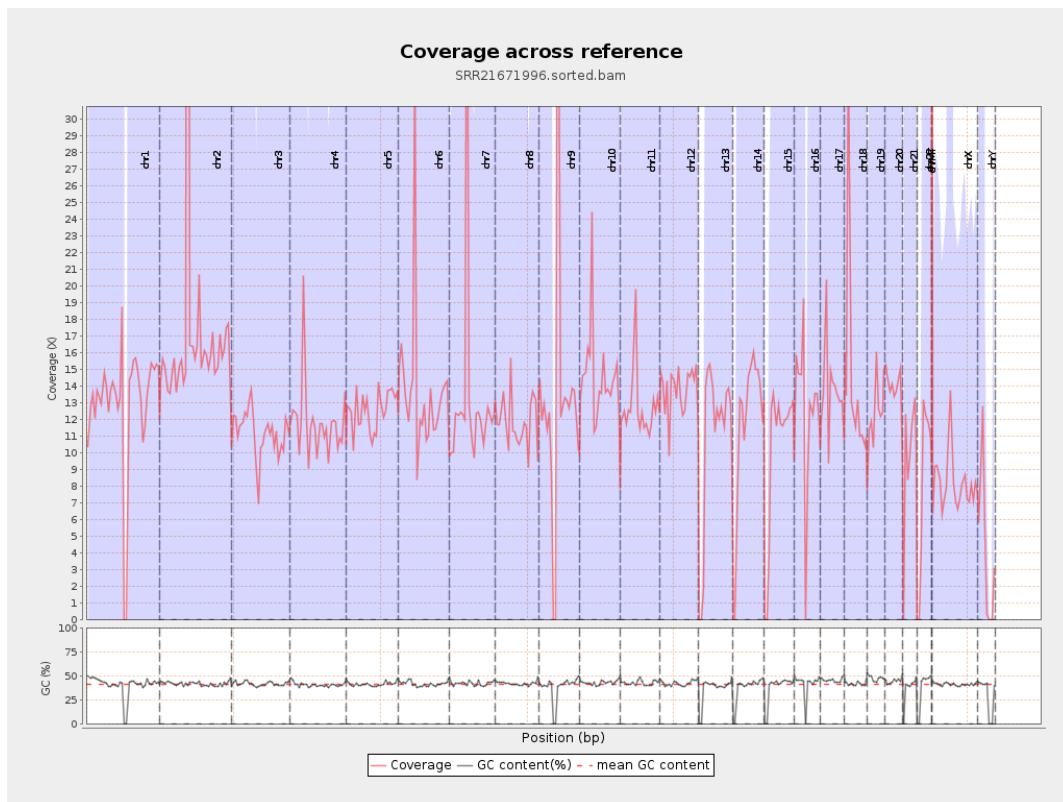
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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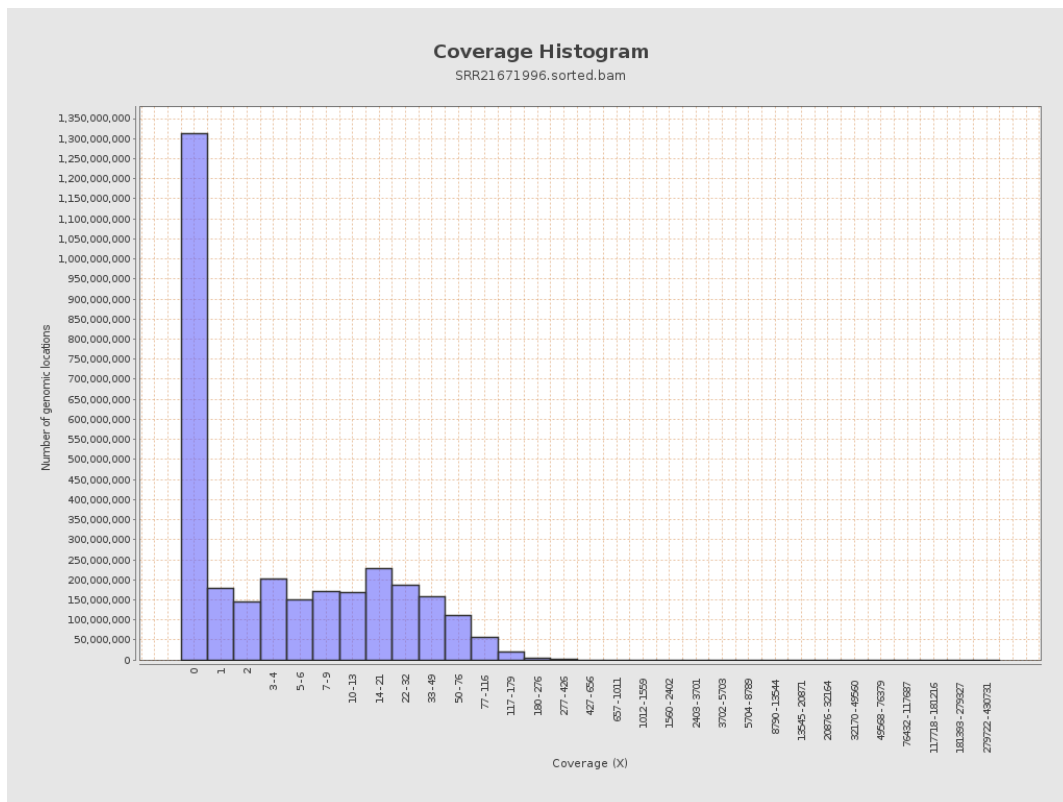
		bases	coverage	deviation
chr1	249250621	3236250627	12.9839	95.2281
chr2	243199373	4460319925	18.3402	473.3288
chr3	198022430	2217172379	11.1966	22.5483
chr4	191154276	2246753782	11.7536	65.0664
chr5	180915260	2268799323	12.5407	27.912
chr6	171115067	2359553218	13.7893	268.5997
chr7	159138663	2117259203	13.3045	576.3099
chr8	146364022	1728438888	11.8092	64.925
chr9	141213431	1855290153	13.1382	694.2301
chr10	135534747	1985675708	14.6507	142.4539
chr11	135006516	1707220327	12.6455	164.1829
chr12	133851895	1840953274	13.7537	28.8591
chr13	115169878	1265117774	10.9848	23.4044
chr14	107349540	1251586101	11.659	28.8722
chr15	102531392	1025400152	10.0008	21.7971
chr16	90354753	1113685875	12.3257	78.7851
chr17	81195210	1111036650	13.6835	139.6946
chr18	78077248	1118585628	14.3267	428.5706
chr19	59128983	725769343	12.2743	103.157
chr20	63025520	881913022	13.993	32.5602
chr21	48129895	479343374	9.9594	53.1852
chr22	51304566	424959798	8.2831	33.799
chrMT	16571	1874276	113.1058	330.6999
chrX	155270560	1265430237	8.1498	57.8136

chrY	59373566	265709483	4.4752	52.4298
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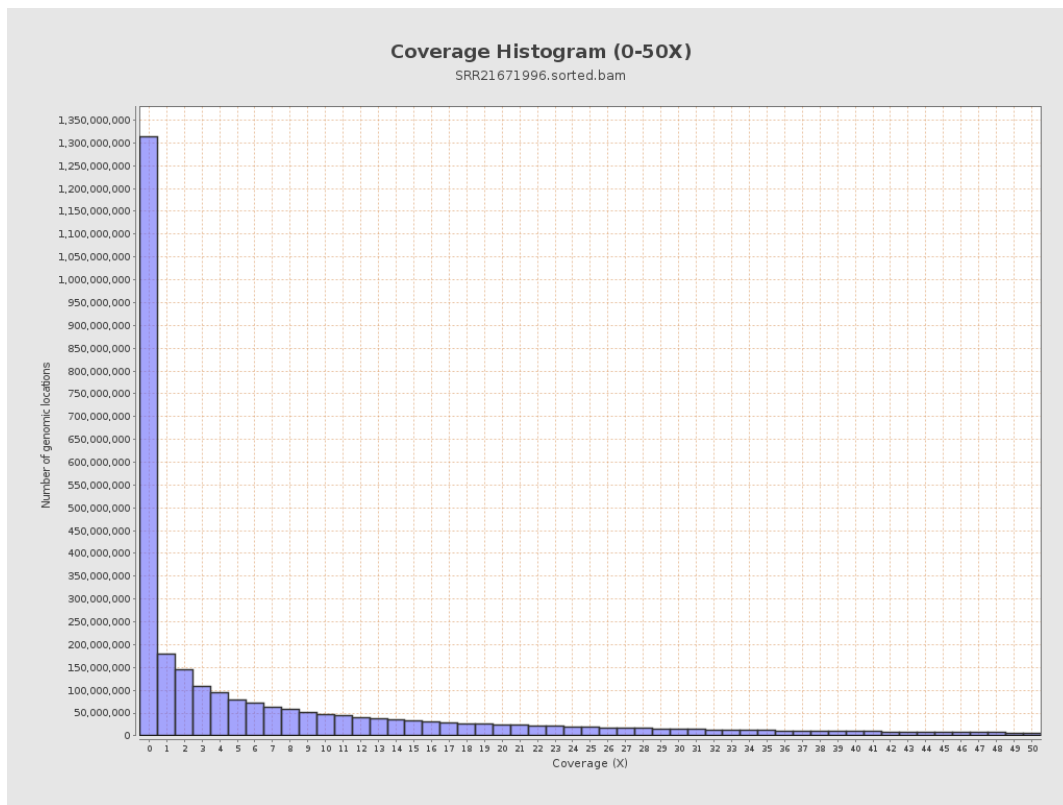
3. Results : Coverage across reference



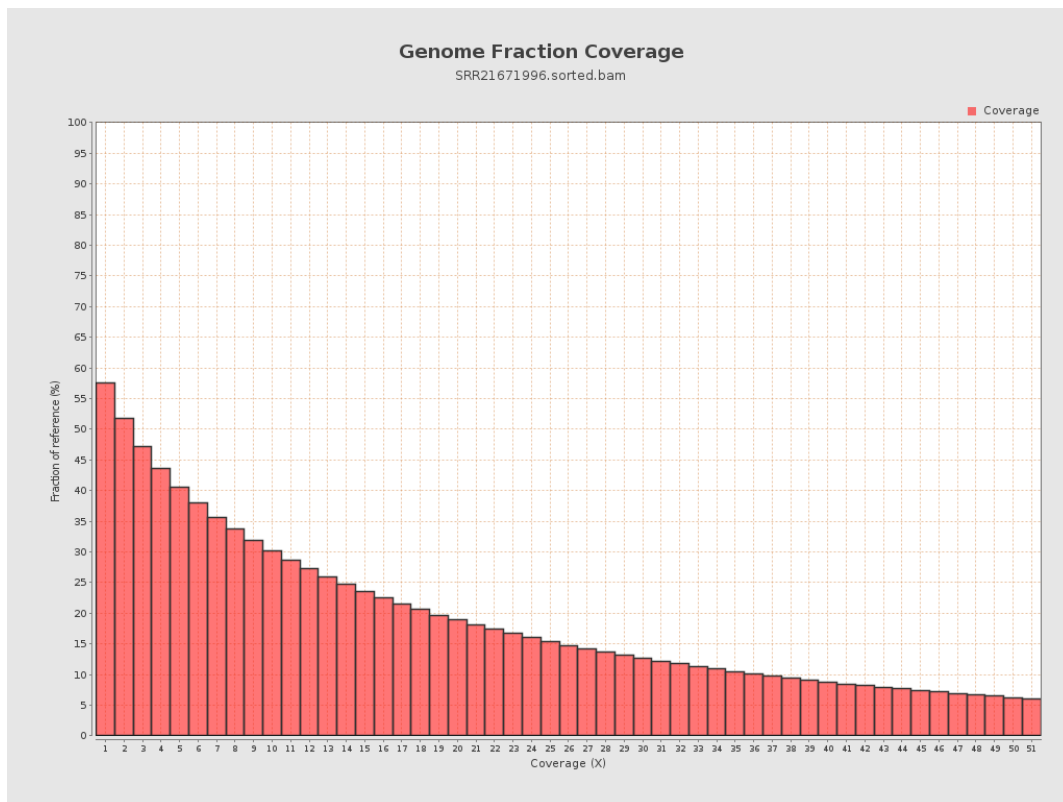
4. Results : Coverage Histogram



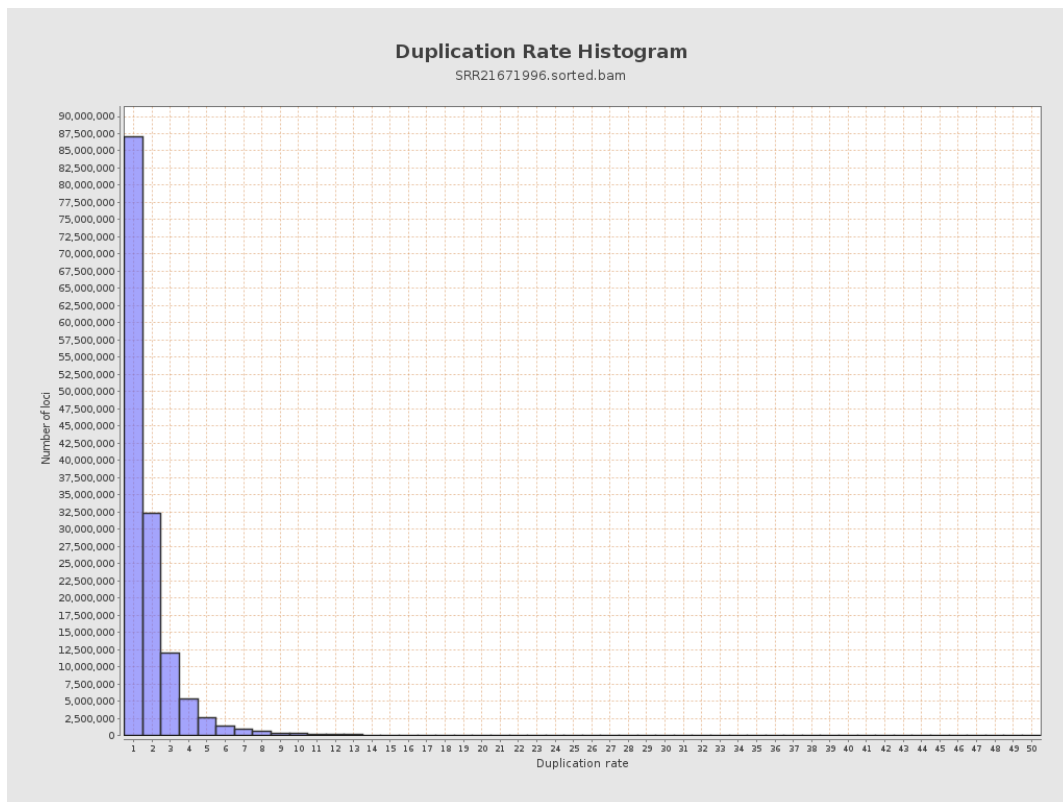
5. Results : Coverage Histogram (0-50X)



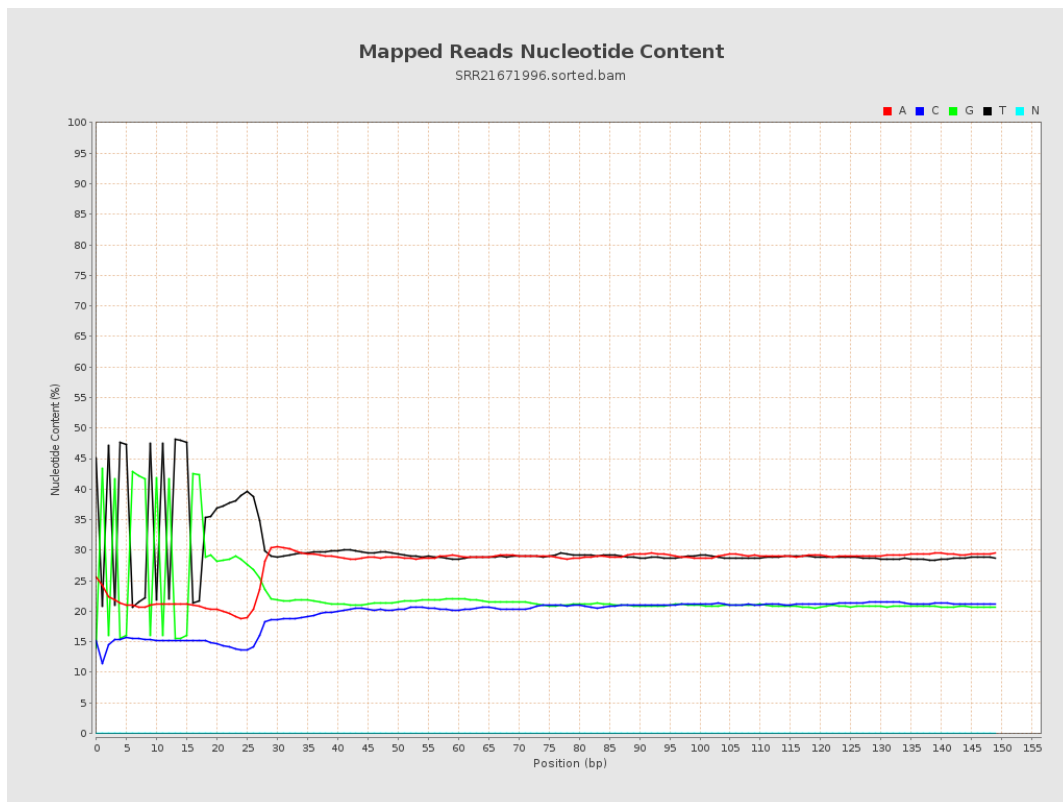
6. Results : Genome Fraction Coverage



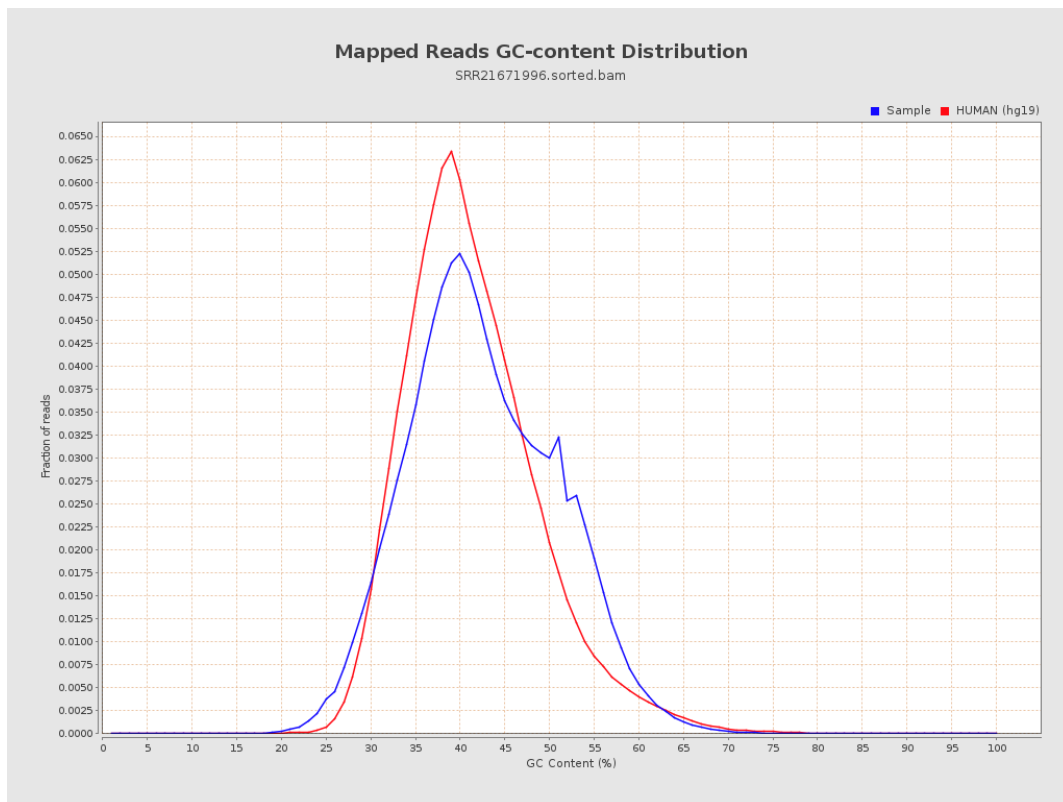
7. Results : Duplication Rate Histogram



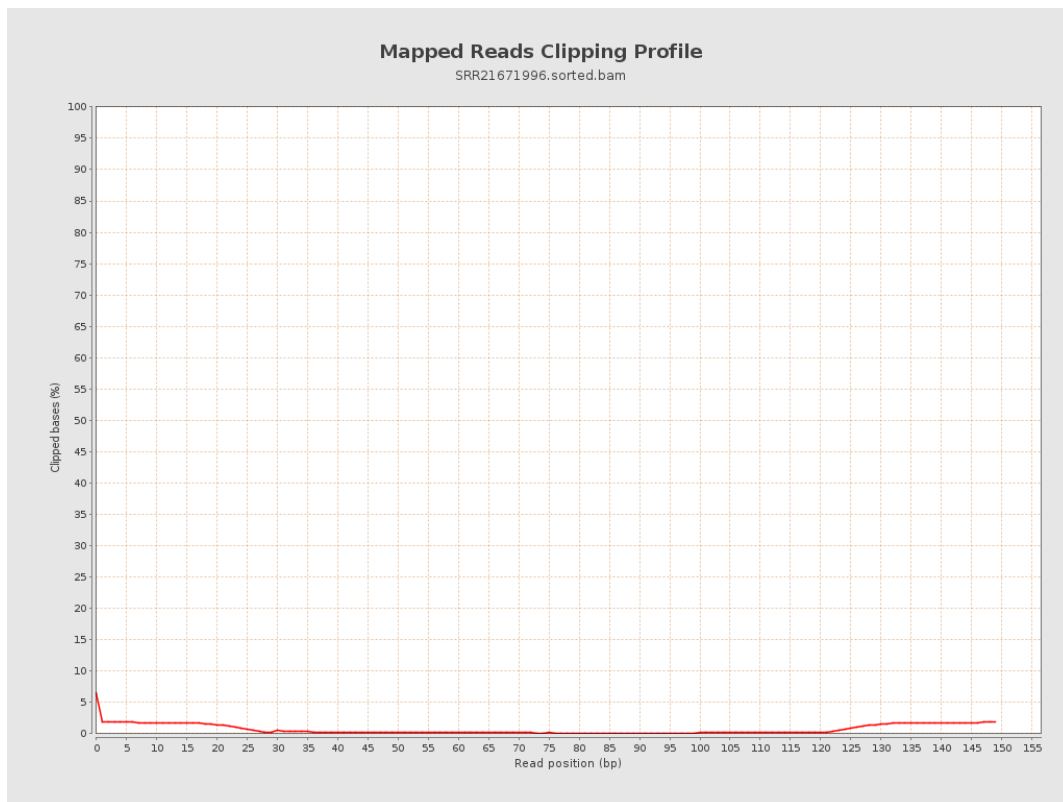
8. Results : Mapped Reads Nucleotide Content



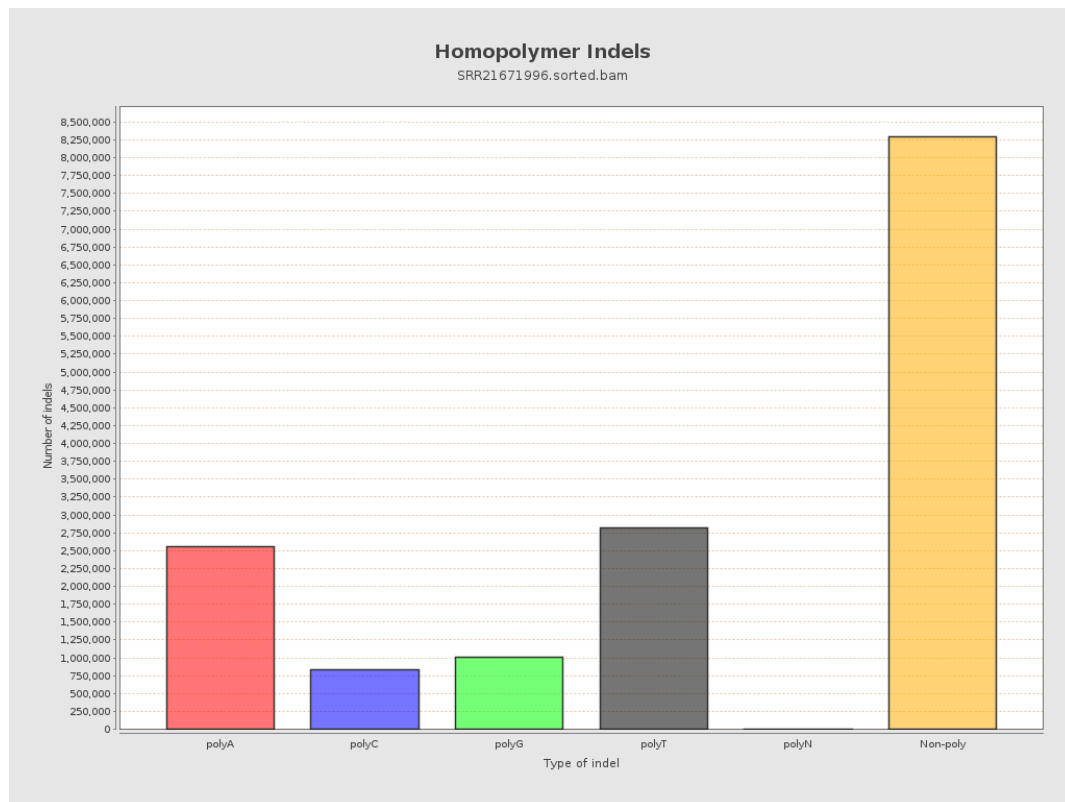
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



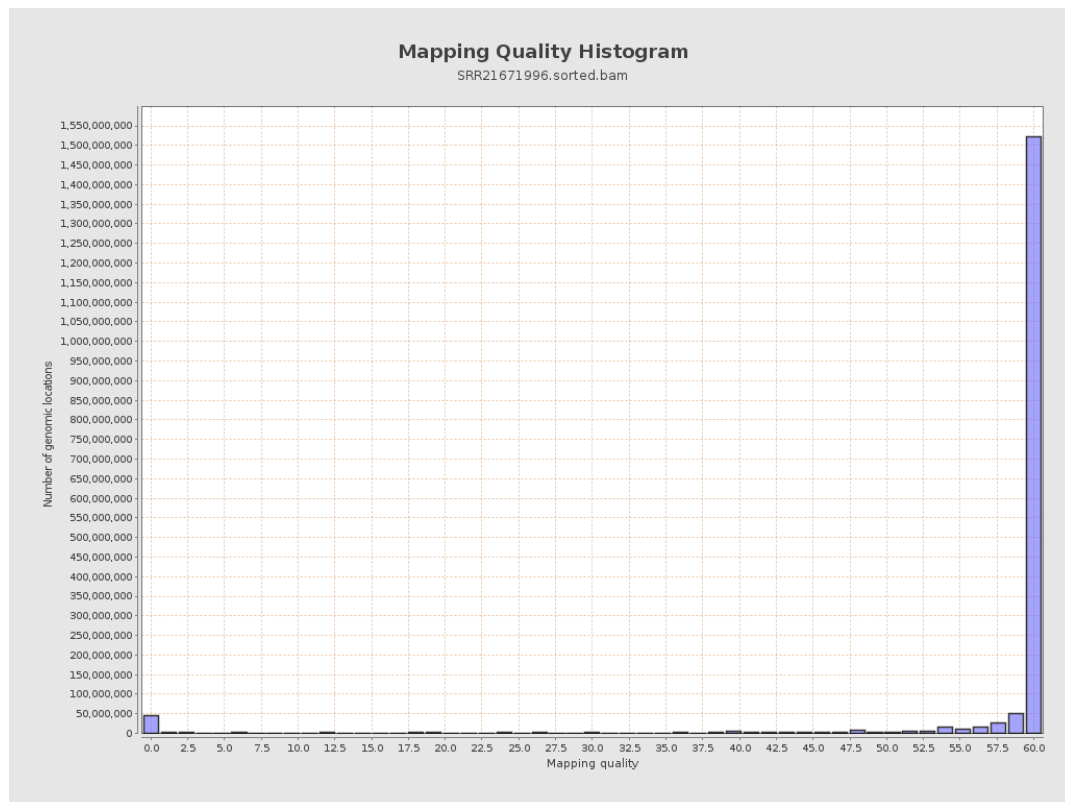
11. Results : Homopolymer Indels



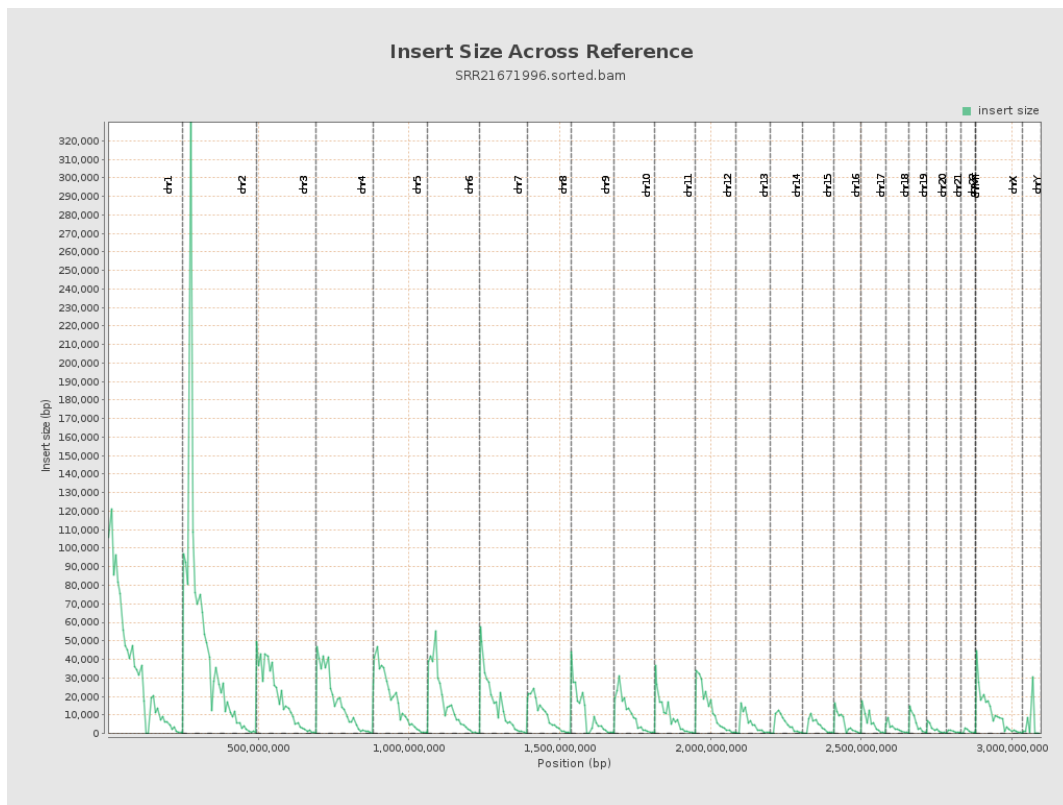
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

